Diabete_prediction_models

March 13, 2025

1 DIABETE PREDICTION

1.0.1 Global Importation

[10]:
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm

from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import␣
 ↪r2_score,mean_squared_error,accuracy_score,confusion_matrix,␣
 ↪classification_report
# VIF
from statsmodels.stats.outliers_influence import variance_inflation_factor
from sklearn.ensemble import␣
 ↪RandomForestClassifier,AdaBoostClassifier,GradientBoostingClassifier
from sklearn.linear_model import LogisticRegression
# RN
import tensorflow as tf
from tensorflow import keras
from keras.models import Sequential
from keras.layers import Dense
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn import datasets
#
from sklearn.neighbors import KNeighborsClassifier
from sklearn.svm import SVC
import numpy as np
from sklearn.model_selection import GridSearchCV
```

1.0.2 Global functions

[11]:
```
def show_graphics(df:pd.DataFrame,target_col):
  variables = df.columns.to_list()
  variables.remove(target_col)

  plt.figure(figsize=(15, 5))
  #Changed the line below to iterate over variables instead of df.columns
  for i, var in enumerate(variables):
      plt.subplot(1, len(variables), i + 1)
      colors = ['blue' if d == 0 else 'red' for d in df[target_col]]
      plt.scatter(df[var], df[target_col], c=colors, alpha=0.7, edgecolor='k',␣
 ↪s=100)
      plt.title(f"{var} vs {target_col}")
      plt.xlabel(var)
      plt.ylabel(target_col)
      plt.grid(True)

  plt.tight_layout()
  plt.show()

def show_corr_matrix(df:pd.DataFrame):
    plt.figure(figsize=(10, 8))
    sns.heatmap(df.corr(), annot=True, cmap='coolwarm', fmt=".2f", linewidths=0.
 ↪5)
    plt.title("Correlation Matrice ")
    plt.show()

def plot_bar_and_pie(data:pd.DataFrame, column:str, figsize=(12,␣
 ↪6),bar_title="Repartition of ",pie_title="Repartition of "):
    """
    Affiche un graphique en barres et un camembert côte à côte
    pour une colonne donnée d'un DataFrame.

    Parameters:
    - data (DataFrame): Le DataFrame contenant les données.
    - column (str): Le nom de la colonne à analyser.
    - figsize (tuple): Taille de la figure (par défaut (12, 6)).
    """
    counts = data[column].value_counts()  # Comptage des valeurs

    # Création de la figure avec deux sous-graphiques
    fig, axes = plt.subplots(1, 2, figsize=figsize)

    # Graphique en barres
    axes[0].bar(x=[str(x) for x in counts.index], height=counts)
    axes[0].set_title(f"{bar_title} {column} (Barres)")
```

```
    axes[0].set_xlabel(column)
    axes[0].set_ylabel('Total')

    # Graphique en camembert
    axes[1].pie(counts, labels=counts.index, autopct='%1.2f%%', explode=[0.2] +␣
 ↪[0] * (len(counts) - 1))
    axes[1].set_title(f" {pie_title} {column} (Camembert)")

    # Ajustement des espaces
    plt.tight_layout()
    plt.show()


#Find the best one variable
def select_best_variable(data,target_col):
    data=data.copy(deep=True)
    r_squared = 0
    y_Y=data[target_col]
    data.drop(target_col,axis=1,inplace=True)
    for x in data.columns[2:] :
        X = data[x]  # Select the column containing the predictive variable
        X = sm.add_constant(X)  # add a constant column for the constant term␣
 ↪of the model (for the parameter beta_0)
        Y = y_Y # Select the target varibale and store it in Y
        model1 = sm.OLS(Y,X).fit() # fit the model to predict Y using X
        if model1.rsquared > r_squared :
            r_squared = model1.rsquared
            m=model1
            x_best = x
    print("The best variable",x_best)
    return m.summary()

def select_best_variables_with_regression(data,target_col):
    data=data.copy(deep=True)
    # Séparer les variables dépendantes et indépendantes
    y = data[target_col]
    X = data.drop(target_col, axis=1)
    # Créer le modèle de régression linéaire
    regressor = LinearRegression()
    # Diviser les données en ensembles de formation et de test
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state=0)
    # Sélectionner les variables les plus importantes
    selected_features = []
    for feature in X_train.columns:
        # Créer un sous-ensemble de variables
        features_subset = selected_features + [feature]
```

```
        # Entraîner le modèle sur le sous-ensemble de variables
        regressor.fit(X_train[features_subset], y_train)
        y_pred = regressor.predict(X_test[features_subset])

        # Calculer le R² ajusté pour le modèle
        r2 = r2_score(y_test, y_pred)
        adj_r2 = 1 - (1 - r2) * (len(y_test) - 1) / (len(y_test) -␣
 ↪len(features_subset) - 1)

        # Ajouter la variable si le R² ajusté a augmenté
        if len(selected_features) == 0 or adj_r2 > max_r2:
            max_r2 = adj_r2
            best_feature = feature
        selected_features.append(best_feature)
    print("Variables sélectionnées : ", selected_features)
    return selected_features

#Modèles non linéaires
def add_polynomial_feature(data1, idx_p, power):
    new_data = data1.copy(deep = True)
    # print("len::",len(idx_p))
    for i in range(0, len(idx_p)):
        for j in power:
            for k in range(2, j+1):
                new_data['{}_pow_{}'.format(idx_p[i],k)] = new_data.loc[:
 ↪,idx_p[i]]**k
    return (new_data)

# Multiple regression
def multiple_regression(data,target_col):
    data=data.copy(deep=True)
    X = data.drop(target_col, axis=1)
    y = data[target_col]
    X = sm.add_constant(X)
    Y = data[target_col]
    model = sm.OLS(Y,X).fit()
    return model.summary()

# VIF verrification
def verify_vif(data,target_col):
    data=data.copy(deep=True)
    X = data.drop(target_col, axis=1)
    X = sm.add_constant(X)  # Ajoute l'intercept

    # Calcul du VIF pour chaque feature
    vif_data = pd.DataFrame()
```

```
    vif_data["Feature"] = X.columns
    vif_data["VIF"] = [variance_inflation_factor(X.values, i) for i in range(X.
 ↪shape[1])]
    return vif_data


# Select feature with Random Forest
def feature_selection_with_rf(data, target, n_features=10, n_estimators=100,␣
 ↪random_state=42):
    # Séparer les features et la cible
    X = data.drop(columns=[target])
    y = data[target]

    # Diviser les données en train, validation et test
    X_train, X_temp, y_train, y_temp = train_test_split(X, y, test_size=0.3,␣
 ↪random_state=random_state)
    X_val, X_test, y_val, y_test = train_test_split(X_temp, y_temp, test_size=0.
 ↪5, random_state=random_state)

    # Initialiser le Random Forest
    rf = RandomForestClassifier(n_estimators=n_estimators,␣
 ↪random_state=random_state)

    # Entraîner le modèle
    rf.fit(X_train, y_train)

    # Prédictions et évaluation sur l'ensemble de validation
    y_val_pred = rf.predict(X_val)
    val_accuracy = accuracy_score(y_val, y_val_pred)
    print(f'Accuracy on validation set: {val_accuracy:.4f}')

    # Prédictions et évaluation sur l'ensemble de test
    y_test_pred = rf.predict(X_test)
    test_accuracy = accuracy_score(y_test, y_test_pred)
    print(f'Accuracy on test set: {test_accuracy:.4f}')

    # Importance des features
    feature_importances = pd.DataFrame({'Feature': X.columns, 'Importance': rf.
 ↪feature_importances_})
    feature_importances = feature_importances.sort_values(by='Importance',␣
 ↪ascending=False)

    # Afficher les features les plus importantes
    print(feature_importances.head(n_features))

    # Sélectionner les meilleures features
```

```
    selected_features = feature_importances.head(n_features)['Feature'].tolist()

    return selected_features
```

0. Load data

[15]:
```
df=pd.read_csv("/home/peyanan/Diabete_prediction/TAIPEI_diabetes.
↪csv",delimiter=",")
```

[16]:
```
df.head(10)
```

[16]:

	PatientID	Pregnancies	PlasmaGlucose	DiastolicBloodPressure	\
0	1354778	0	171	80	
1	1147438	8	92	93	
2	1640031	7	115	47	
3	1883350	9	103	78	
4	1424119	1	85	59	
5	1619297	0	82	92	
6	1660149	0	133	47	
7	1458769	0	67	87	
8	1201647	8	80	95	
9	1403912	1	72	31	

	TricepsThickness	SerumInsulin	BMI	DiabetesPedigree	Age	Diabetic
0	34	23	43.509726	1.213191	21	0
1	47	36	21.240576	0.158365	23	0
2	52	35	41.511523	0.079019	23	0
3	25	304	29.582192	1.282870	43	1
4	27	35	42.604536	0.549542	22	0
5	9	253	19.724160	0.103424	26	0
6	19	227	21.941357	0.174160	21	0
7	43	36	18.277723	0.236165	26	0
8	33	24	26.624929	0.443947	53	1
9	40	42	36.889576	0.103944	26	0

2 1. Data comprehension

2.0.1 1.1 Data size

[17]:
```
# Data size
df.shape
```

[17]:
```
(15000, 10)
```

NB: According data set size,we get:

- 15K rows
- 10 columns

1.2. Columns's type analysis

[18]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 15000 entries, 0 to 14999
Data columns (total 10 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   PatientID               15000 non-null  int64
 1   Pregnancies             15000 non-null  int64
 2   PlasmaGlucose           15000 non-null  int64
 3   DiastolicBloodPressure  15000 non-null  int64
 4   TricepsThickness        15000 non-null  int64
 5   SerumInsulin            15000 non-null  int64
 6   BMI                     15000 non-null  float64
 7   DiabetesPedigree        15000 non-null  float64
 8   Age                     15000 non-null  int64
 9   Diabetic                15000 non-null  int64
dtypes: float64(2), int64(8)
memory usage: 1.1 MB
```

NB 1.2: Accord this part, there are two types of columns:

- Integer: All columns except BMI and DiabetesPedigree
- Float:BMI,DiabetesPedigree
- Type base: 64

We can also mark, there are no missing value because we are the same size with our original data set. Howover, we have to verify with another Method in the step.

1.3 A few statistics

[19]:
```
# Analyzing descriptive statistics
df.describe()
```

[19]:

	PatientID	Pregnancies	PlasmaGlucose	DiastolicBloodPressure	\
count	1.500000e+04	15000.000000	15000.000000	15000.000000	
mean	1.502922e+06	3.224533	107.856867	71.220667	
std	2.892534e+05	3.391020	31.981975	16.758716	
min	1.000038e+06	0.000000	44.000000	24.000000	
25%	1.252866e+06	0.000000	84.000000	58.000000	
50%	1.505508e+06	2.000000	104.000000	72.000000	
75%	1.755205e+06	6.000000	129.000000	85.000000	
max	1.999997e+06	14.000000	192.000000	117.000000	

	TricepsThickness	SerumInsulin	BMI	DiabetesPedigree	\
count	15000.000000	15000.000000	15000.000000	15000.000000	
mean	28.814000	137.852133	31.509646	0.398968	
std	14.555716	133.068252	9.759000	0.377944	

```
min            7.000000     14.000000     18.200512          0.078044
25%           15.000000     39.000000     21.259887          0.137743
50%           31.000000     83.000000     31.767940          0.200297
75%           41.000000    195.000000     39.259692          0.616285
max           93.000000    799.000000     56.034628          2.301594

                Age      Diabetic
count  15000.000000  15000.000000
mean      30.137733      0.333333
std       12.089703      0.471420
min       21.000000      0.000000
25%       22.000000      0.000000
50%       24.000000      0.000000
75%       35.000000      1.000000
max       77.000000      1.000000
```

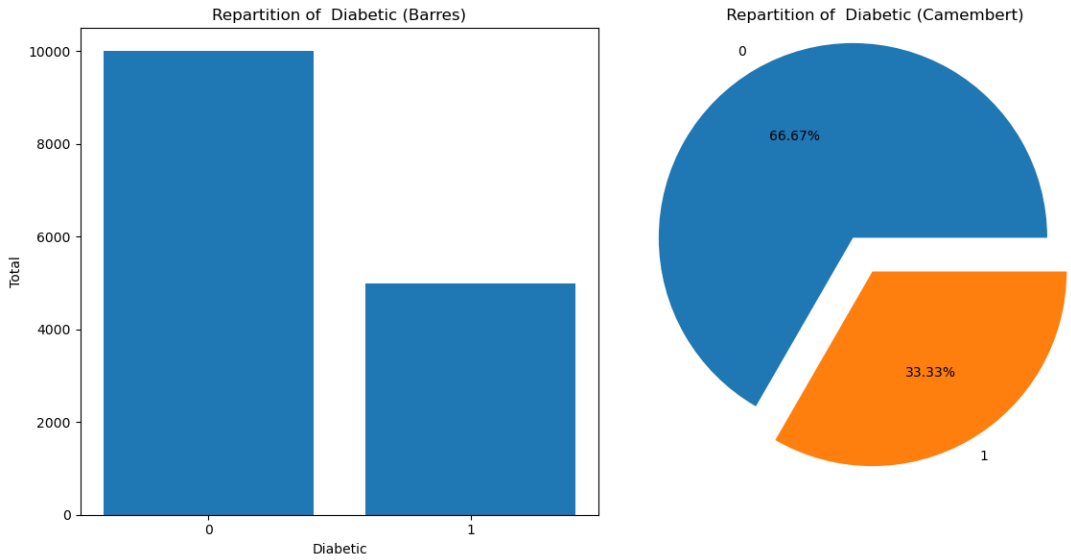
[20]:
```
# Show if we have missing data.
messing=f"isna:{df.isna().sum()} ␣
 ↪\n|=========================================| \n isnull:{df.isnull().
 ↪sum()}"
print(messing)
```

```
isna:PatientID                0
Pregnancies                   0
PlasmaGlucose                 0
DiastolicBloodPressure        0
TricepsThickness              0
SerumInsulin                  0
BMI                           0
DiabetesPedigree              0
Age                           0
Diabetic                      0
dtype: int64
|=========================================|
 isnull:PatientID                0
Pregnancies                   0
PlasmaGlucose                 0
DiastolicBloodPressure        0
TricepsThickness              0
SerumInsulin                  0
BMI                           0
DiabetesPedigree              0
Age                           0
Diabetic                      0
dtype: int64
```

[21]:
```
# Show number of diabetes diagnosed in our data dataset
diagnosed=df['Diabetic'].value_counts()
diagnosed_percentage = df['Diabetic'].value_counts(normalize=True) * 100
print("Diagnosed:",diagnosed)
print("Percentage:",diagnosed_percentage)
```

```
Diagnosed: Diabetic
0    10000
1     5000
Name: count, dtype: int64
Percentage: Diabetic
0    66.666667
1    33.333333
Name: proportion, dtype: float64
```

[22]:
```
plot_bar_and_pie(df,"Diabetic")
```




```
NB:
 - Looking at these statistics, no data is missing. Moreover, there is no categorical data.
 - In this data set, 33,33% either 5k persons have a diabete again 66,33% either 10k no diagnos
```

2.1 2. Analyzing of data features

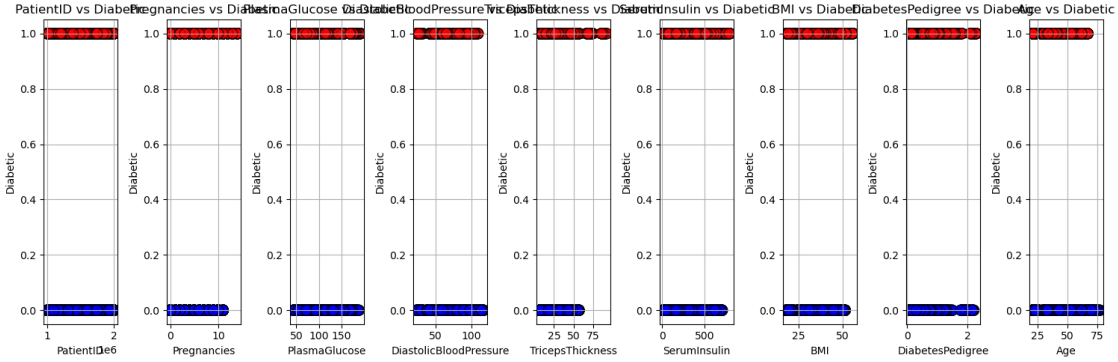
- PatientID :Is a patient identifier.
- Pregnancies:Number of times pregnant.
- PlasmaGlucose: Plasma glucose concentration after 2 hours in an oral glucose tolerance test.
- DiastolicBloodPressure:A function that scores the probability of diabetes based on family history.
- TricepsThickness:Triceps skin fold thickness (mm).

- SerumInsulin:2-Hour serum insulin (mu U/ml).
- BMI: Body mass index (weight in kg/(height in m)^2).
- DiabetesPedigree:A function that scores the probability of diabetes based on family history.
- Age:Age in years the species.
- Diabetic:Is the truth, the goal for Prediction.

2.1.1 2.1. Visualization of the point cloud.

A. Show a relationship between each feature with our target and catch outlier as possible.

[23]:
```
show_graphics(df,'Diabetic')
```

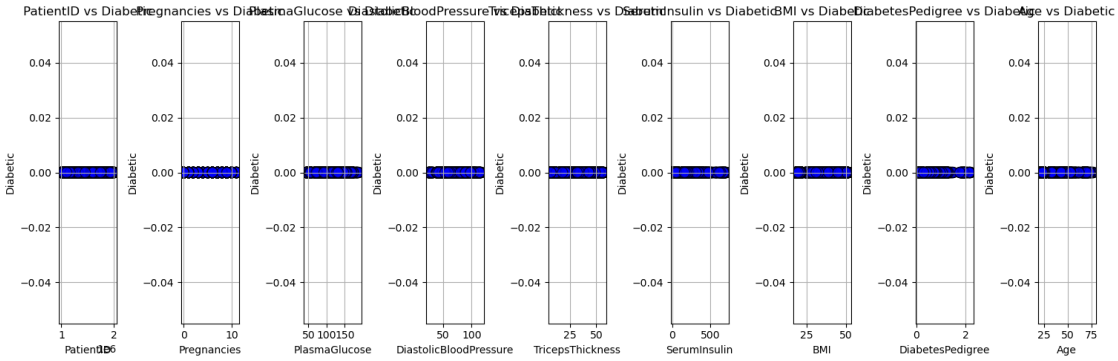


B. Show a relationship between each feature with our target spliting by cluster (0 and 1) and catch outlier as possible.

[24]:
```
no_diabete_df=df[df['Diabetic']==0]
diabete_df=df[df['Diabetic']==1]
```

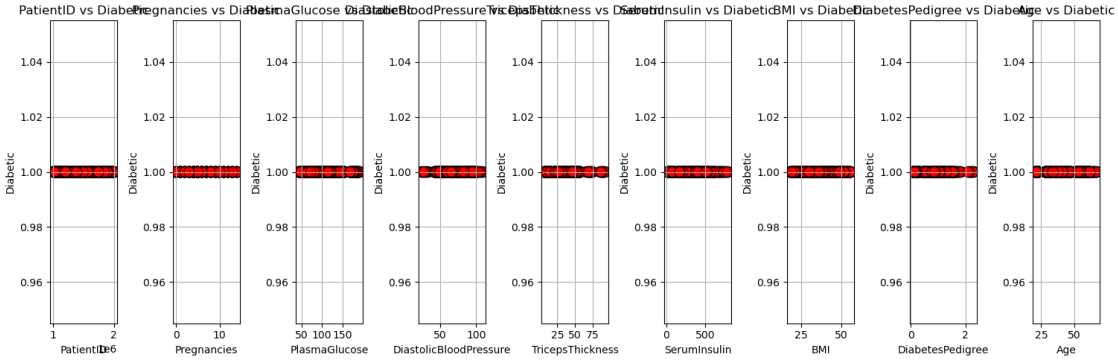
- No diabete cloud points

[25]:
```
show_graphics(no_diabete_df,'Diabetic')
```



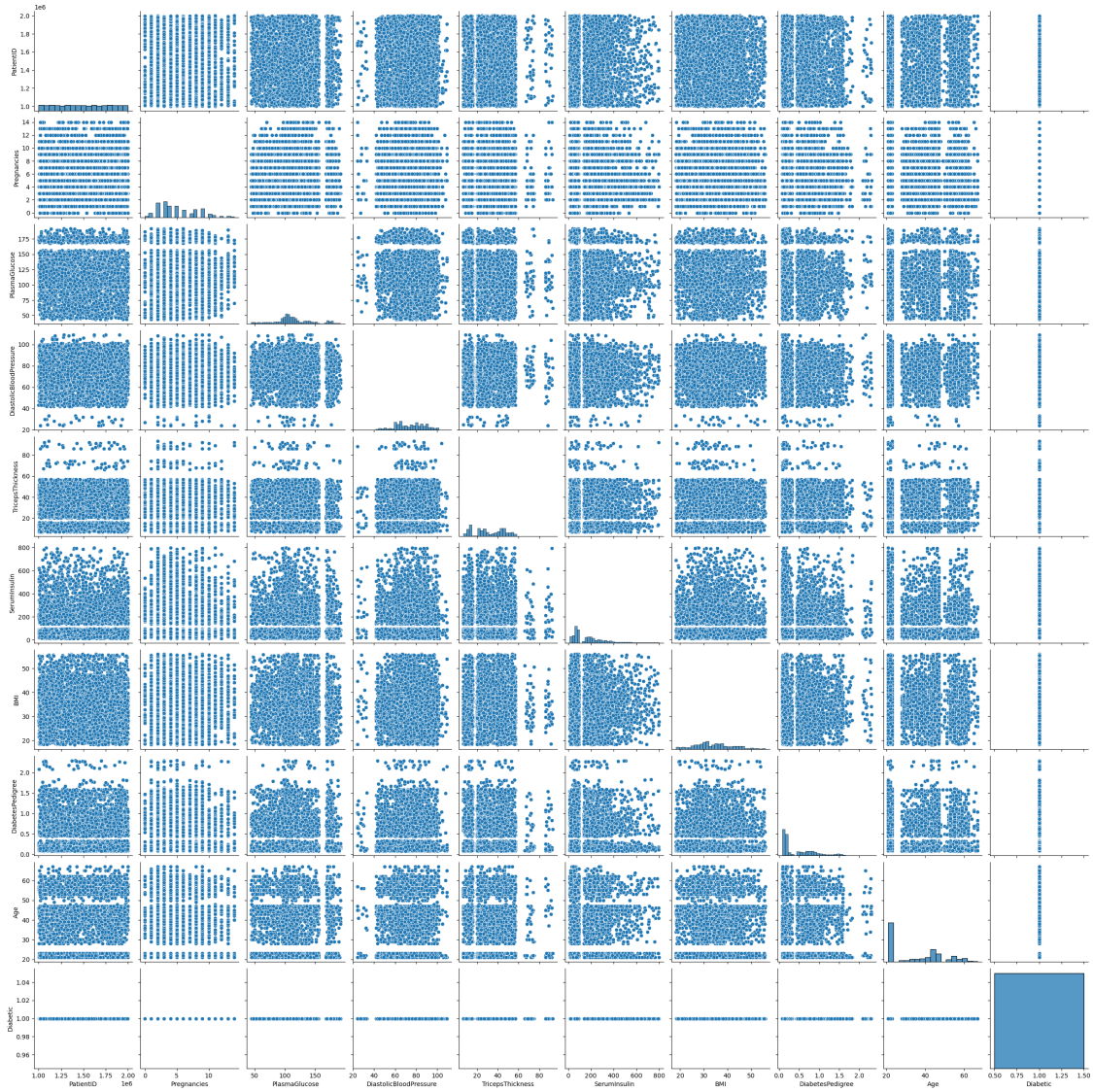
- Diabete cloud points

[26]:
```
show_graphics(diabete_df,'Diabetic')
```



Distribution of each feature

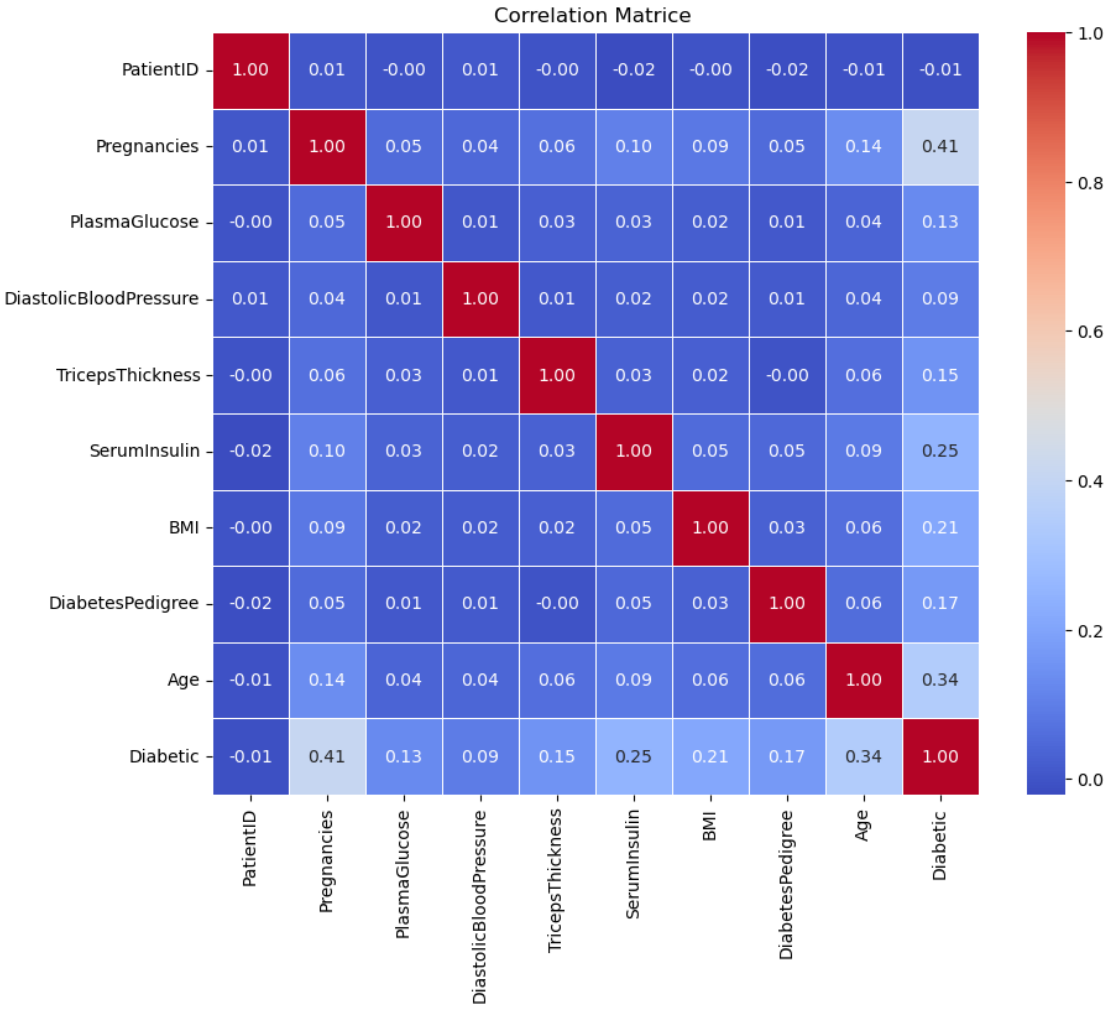
[27]:
```
sns.pairplot(diabete_df)
plt.show()
```



C. Feature relationship with correlation

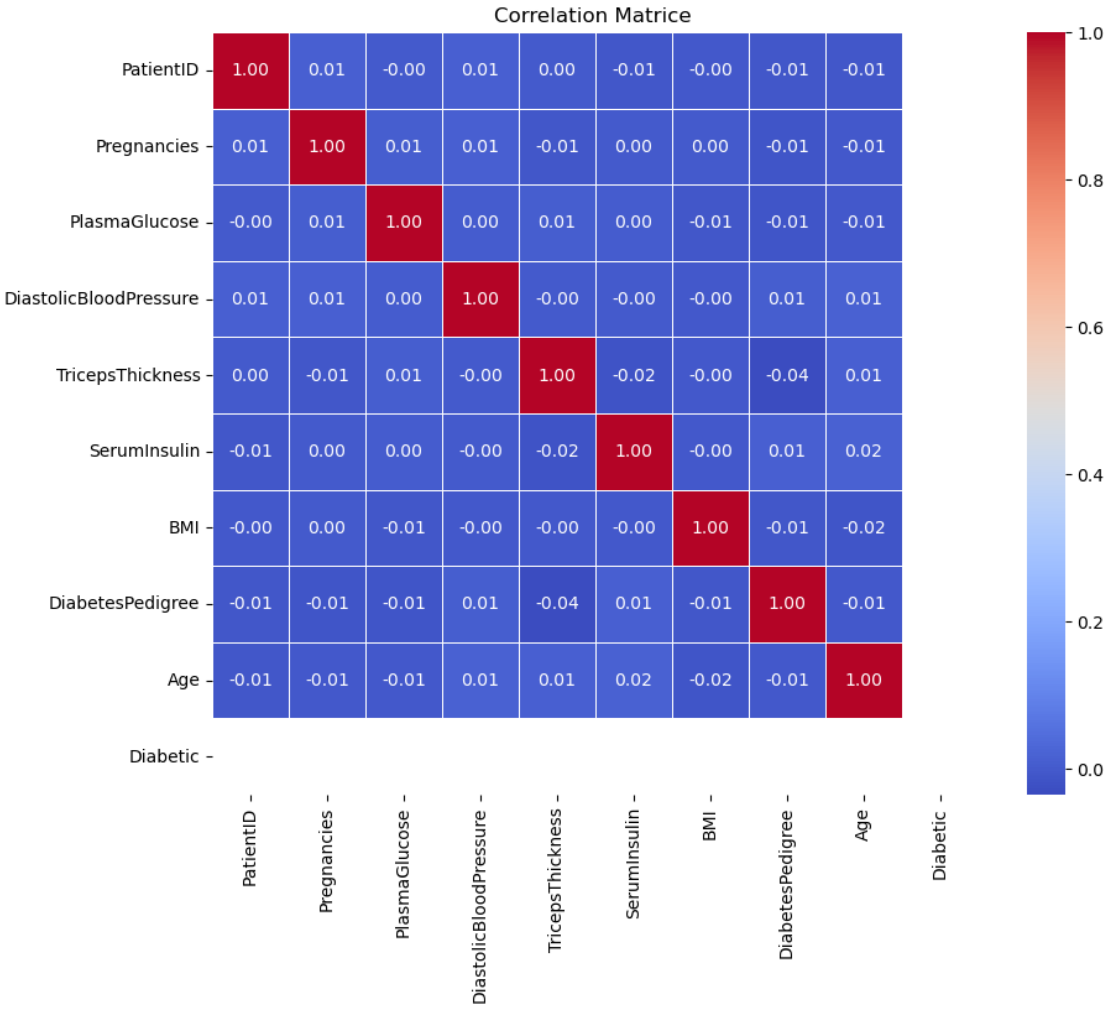
- All cluster (0 and 1) correlation.

[28]:
```
# correlation_matrix = df.corr()
# print(correlation_matrix)
# Corr
show_corr_matrix(df)
```



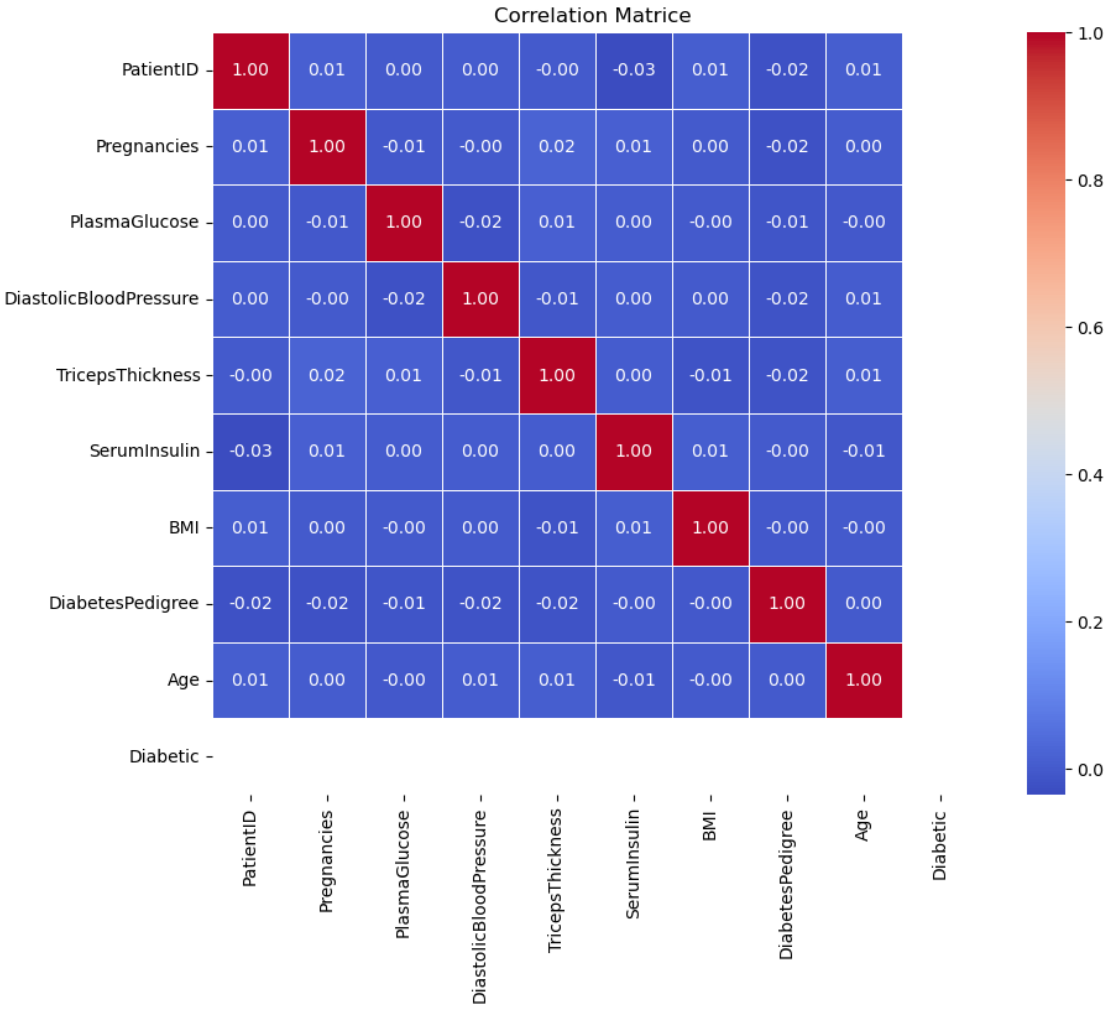
- Cluster (0) correlation.

[29]:
```
show_corr_matrix(no_diabete_df)
```



- Cluster (1) correlation.

[30]:
```
show_corr_matrix(diabete_df)
```



2.1.2 NB-RESUME:

In summary, after this analysis, it is clear that the "PatientID" variable is of no use in our study. Furthermore, the correlations with the target are generally very weak, with the exception of that with the "Pregnancies" variable. This low or non-existent correlation clearly indicates that our variables are independent of each other. This eliminates the need for a **Decorrelation** step through dimension reduction techniques, such as PCA or PCA.

This leads us to formulate the following hypotheses:

- All variables, with the exception of "PatientID", contribute to the explanation of the target variable "Diabetic".
- The variable "Pregnancies", which shows the strongest correlation with "Diabetic", seems to play a significant role in explaining the target.
- The "PlasmaGlucose", "BMI" and "Age" variables are strongly linked to known metabolic factors. They could have a significant influence on "Diabetic", although their direct correla-

tions are weak.

- The variables “PatientID” and “DiastolicBloodPressure” provide no significant information to explain “Diabetic” and can be excluded without affecting model performance.

Note: In order to validate these hypotheses, statistical tests will be carried out to select the relevant variables, then a series of models will be created to choose the one offering the best performance.

2.1.3 2-1) Features selections

-

[31]:
```
best_variable=select_best_variable(df,"Diabetic")
```

```
The best variable Age
```

[32]:
```
df.columns
```

[32]:
```
Index(['PatientID', 'Pregnancies', 'PlasmaGlucose', 'DiastolicBloodPressure',
       'TricepsThickness', 'SerumInsulin', 'BMI', 'DiabetesPedigree', 'Age',
       'Diabetic'],
      dtype='object')
```

[33]:
```
best_variables=select_best_variables_with_regression(df,"Diabetic")
```

```
Variables sélectionnées :  ['PatientID', 'Pregnancies', 'PlasmaGlucose',
'DiastolicBloodPressure', 'TricepsThickness', 'SerumInsulin', 'BMI',
'DiabetesPedigree', 'Age']
```

[34]:
```
summary=multiple_regression(df,"Diabetic")
print(summary)
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                Diabetic   R-squared:                       0.345
Model:                            OLS   Adj. R-squared:                  0.345
Method:                 Least Squares   F-statistic:                     879.0
Date:                Wed, 12 Mar 2025   Prob (F-statistic):               0.00
Time:                        12:06:20   Log-Likelihood:                -6825.0
No. Observations:               15000   AIC:                         1.367e+04
Df Residuals:                   14990   BIC:                         1.375e+04
Df Model:                           9
```

```
Covariance Type:            nonrobust
==============================================================================
==========
                             coef    std err          t      P>|t|      [0.025
0.975]
------------------------------------------------------------------------------
----------
const                     -0.8165      0.027    -30.350      0.000      -0.869
-0.764
PatientID              -1.144e-08   1.08e-08     -1.062      0.288   -3.26e-08
9.68e-09
Pregnancies                0.0446      0.001     47.594      0.000       0.043
0.046
PlasmaGlucose              0.0013   9.77e-05     13.191      0.000       0.001
0.001
DiastolicBloodPressure     0.0016      0.000      8.620      0.000       0.001
0.002
TricepsThickness           0.0034      0.000     15.792      0.000       0.003
0.004
SerumInsulin               0.0006   2.37e-05     25.529      0.000       0.001
0.001
BMI                        0.0072      0.000     22.416      0.000       0.007
0.008
DiabetesPedigree           0.1558      0.008     18.829      0.000       0.140
0.172
Age                        0.0099      0.000     37.959      0.000       0.009
0.010
==============================================================================
Omnibus:                      511.711   Durbin-Watson:                   2.016
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              444.799
Skew:                           0.358   Prob(JB):                     2.59e-97
Kurtosis:                       2.555   Cond. No.                     1.32e+07
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 1.32e+07. This might indicate that there are
strong multicollinearity or other numerical problems.
```

Conclusion for linear feature selection: As we can see above ,

About the model quality : - **R=0.345**, This model explain only 34,5% of the variance of the target variable ("Diabetic").So more than 70% diabetic case is not explain. - F-statistic = 694.7, Prob (F-statistic) = 0.00 : The overall model is significant, so at least one of the explanatory variables has an effect on the target variable("Diabetic").

About a feature: All of them is significant except patientID because we have **(P>|t| < 0.05)** for *Pregnancies, PlasmaGlucose, DiastolicBloodPressure, TricepsThickness, SerumInsulin, BMI, DiabetesPedigree and Age.*

According to the Diagnostics ,**Cond. No. = 1.32e+07**: This number is very high, potentially suggesting collinearity problems between the independent variables.. Il faudrait vérifier la matrice de corrélation ou utiliser des outils comme le VIF (Variance Inflation Factor). As this explain only 34% of diabetic case, we will test others strategies

-

Mutiple regression for polinomial feature

[35]:
```
col=df.columns.to_list()
col.remove('Diabetic')
train_poly = add_polynomial_feature(df,col,[2])
```

[36]:
```
print(train_poly.columns)
```

```
Index(['PatientID', 'Pregnancies', 'PlasmaGlucose', 'DiastolicBloodPressure',
       'TricepsThickness', 'SerumInsulin', 'BMI', 'DiabetesPedigree', 'Age',
       'Diabetic', 'PatientID_pow_2', 'Pregnancies_pow_2',
       'PlasmaGlucose_pow_2', 'DiastolicBloodPressure_pow_2',
       'TricepsThickness_pow_2', 'SerumInsulin_pow_2', 'BMI_pow_2',
       'DiabetesPedigree_pow_2', 'Age_pow_2'],
      dtype='object')
```

[37]:
```
summary=multiple_regression(train_poly,"Diabetic")
print(summary)
```

```
                            OLS Regression Results
==============================================================================
Dep. Variable:                Diabetic   R-squared:                       0.428
Model:                            OLS   Adj. R-squared:                  0.428
Method:                 Least Squares   F-statistic:                     623.8
Date:                Wed, 12 Mar 2025   Prob (F-statistic):               0.00
Time:                        12:06:20   Log-Likelihood:                -5808.3
No. Observations:               15000   AIC:                         1.165e+04
Df Residuals:                   14981   BIC:                         1.180e+04
Df Model:                          18
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          t      P>|t|      [0.025      0.975]
------------------------------------------------------------------------------
const          -2.4545      0.111    -22.173      0.000
```

```
-2.671      -2.237
PatientID                    -6.211e-08   1.18e-07     -0.528      0.598
-2.93e-07    1.69e-07
Pregnancies                      0.1292      0.003     46.254      0.000
0.124       0.135
PlasmaGlucose                    0.0041      0.001      7.242      0.000
0.003       0.005
DiastolicBloodPressure           0.0193      0.001     14.191      0.000
0.017       0.022
TricepsThickness                -0.0016      0.001     -2.179      0.029
-0.003      -0.000
SerumInsulin                     0.0010   5.74e-05     18.021      0.000
0.001       0.001
BMI                              0.0494      0.002     21.234      0.000
0.045       0.054
DiabetesPedigree                 0.1205      0.021      5.629      0.000
0.079       0.162
Age                              0.0305      0.002     19.437      0.000
0.027       0.034
PatientID_pow_2               1.691e-14    3.9e-14      0.433      0.665
-5.96e-14    9.34e-14
Pregnancies_pow_2               -0.0094      0.000    -33.046      0.000
-0.010      -0.009
PlasmaGlucose_pow_2          -1.288e-05   2.45e-06     -5.248      0.000
-1.77e-05   -8.07e-06
DiastolicBloodPressure_pow_2    -0.0001    9.6e-06    -13.259      0.000
-0.000      -0.000
TricepsThickness_pow_2        7.765e-05   1.18e-05      6.590      0.000
5.46e-05       0.000
SerumInsulin_pow_2           -9.654e-07   1.03e-07     -9.361      0.000
-1.17e-06   -7.63e-07
BMI_pow_2                       -0.0007   3.55e-05    -18.600      0.000
-0.001      -0.001
DiabetesPedigree_pow_2           0.0083      0.014      0.592      0.554
-0.019       0.036
Age_pow_2                       -0.0003   1.97e-05    -13.989      0.000
-0.000      -0.000
==============================================================================
Omnibus:                      268.925   Durbin-Watson:                   2.020
Prob(Omnibus):                  0.000   Jarque-Bera (JB):              185.511
Skew:                           0.159   Prob(JB):                     5.21e-41
Kurtosis:                       2.557   Cond. No.                     9.50e+13
==============================================================================

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly
specified.
[2] The condition number is large, 9.5e+13. This might indicate that there are
```

```
strong multicollinearity or other numerical problems.
```

Conclusion for polinomiale feature $R^2 = 0.428$, Adj. $R^2 = 0.428$: This mean this model explain 42% of the diabetic. It less better than the other above.

Cond. No.(Condition Number) = 9.66e+13: This number is huge, so it's a strong indication of collinearity between variables, especially with the addition of polynomial terms. So the decree 2 polynomial is too much, so the best model is a simple one, which we'll look at next.

Verification of VIF(Variance Inflation Factor #### Cleaning

[38]:
```
# cleaning data:PatientID will be removed
df_cleaned=df.drop('PatientID',axis=1)
```

[39]:
```
vif_data =verify_vif(df_cleaned,"Diabetic")
print(vif_data.sort_values(by="VIF", ascending=False))
```

```
                  Feature        VIF
0                   const  47.373366
1             Pregnancies   1.041960
8                     Age   1.033993
5             SerumInsulin   1.020842
6                     BMI   1.012699
4         TricepsThickness   1.008115
7         DiabetesPedigree   1.007335
2            PlasmaGlucose   1.005320
3  DiastolicBloodPressure   1.003652
```

Note VIF: All the VIFs are very low (around 1), meaning that there is no problematic collinearity between the variables.

Feature selection with random forest

[40]:
```
#feature selection test
selected_features = feature_selection_with_rf(df_cleaned, 'Diabetic',␣
 ↪n_features=10)
print("Features sélectionnées:", selected_features)
```

```
Accuracy on validation set: 0.9329
Accuracy on test set: 0.9338
                  Feature  Importance
0             Pregnancies    0.296301
7                     Age    0.172709
5                     BMI    0.164595
4             SerumInsulin    0.118738
1            PlasmaGlucose    0.095368
3         TricepsThickness    0.056577
2  DiastolicBloodPressure    0.050835
6         DiabetesPedigree    0.044877
Features sélectionnées: ['Pregnancies', 'Age', 'BMI', 'SerumInsulin',
```

```
'PlasmaGlucose', 'TricepsThickness', 'DiastolicBloodPressure',
'DiabetesPedigree']
```

[41]:
```
# with polynomial case
selected_features = feature_selection_with_rf(train_poly, 'Diabetic',␣
 ↪n_features=10)
print("Features sélectionnées:", selected_features)
```

```
Accuracy on validation set: 0.9298
Accuracy on test set: 0.9298
                Feature  Importance
10    Pregnancies_pow_2    0.179629
1           Pregnancies    0.165705
17            Age_pow_2    0.086072
6                   BMI    0.083436
8                   Age    0.083199
15            BMI_pow_2    0.077615
14   SerumInsulin_pow_2    0.056188
5          SerumInsulin    0.049178
2         PlasmaGlucose    0.039526
11  PlasmaGlucose_pow_2    0.037754
Features sélectionnées: ['Pregnancies_pow_2', 'Pregnancies', 'Age_pow_2', 'BMI',
'Age', 'BMI_pow_2', 'SerumInsulin_pow_2', 'SerumInsulin', 'PlasmaGlucose',
'PlasmaGlucose_pow_2']
```

2.1.4 Conclusion Part 2:

The significant features of this dataset for diabetic diagnosis are Pregnancies, Age, BMI, SerumInsulin, PlasmaGlucose, TricepsThickness, DiastolicBloodPressure, and DiabetesPedigree. However, Pregnancies, Age, BMI, and SerumInsulin are more significant than the others. We note that the polynomial feature is not significant as can see in his accurancy of test dataset. That say, the model explain less than 50% of the population (target feature: diabetic).

2.2 3. Data Prediction

3.1. Spliting data set

[42]:
```
# Initial division: training (70%) and temporary set (40%)
train_set, temp_set, train_labels, temp_labels = train_test_split(
    df_cleaned[['Pregnancies', 'PlasmaGlucose', 'DiastolicBloodPressure',
                'TricepsThickness', 'SerumInsulin', 'BMI', 'DiabetesPedigree',␣
 ↪'Age']],
    df_cleaned['Diabetic'],
    test_size=0.3,  # 30% for test + validation
    random_state=42
)

# Division of temporary set: validation (50% of temporary set) and testing (50%␣
 ↪of temporary set)
```

```
validation_set, test_set, validation_labels, test_labels = train_test_split(
    temp_set,
    temp_labels,
    test_size=0.5,  # 50% for  temporaire set
    random_state=42
)
```

[43]:
```
# Displaying set sizes
print("Size of train set :", train_set.shape)
print("Size of validation set:", validation_set.shape)
print("Size of test set:", test_set.shape)
```

```
Size of train set : (10500, 8)
Size of validation set: (2250, 8)
Size of test set: (2250, 8)
```

[44]:
```
# Verification of spliting size
train_set_percentage=train_set.shape[0]/df_cleaned.shape[0]
test_set_percentage=test_set.shape[0]/df_cleaned.shape[0]
validation_set_percentage=validation_set.shape[0]/df_cleaned.shape[0]
print(f"train_set_percentage:{train_set_percentage} \ntest_set_percentage:
 ↪{test_set_percentage} \nvalidation_set_percentage:
 ↪{validation_set_percentage}")
```

```
train_set_percentage:0.7
test_set_percentage:0.15
validation_set_percentage:0.15
```

[45]:
```
# validation_labels
test_labels
```

[45]:
```
8602     0
438      0
8094     0
14355    1
8581     1
        ..
3409     0
6973     1
708      0
3351     1
2142     1
Name: Diabetic, Length: 2250, dtype: int64
```

3.2. Models Creation What task do we have to perform? This is a suppervised task

Case 1: Linear regression

[46]:
```
# Linear regression model initialization
linear_model = LinearRegression()
# Model training
linear_model.fit(train_set, train_labels)
# Prédictions of the  validation set
validation_predictions = linear_model.predict(validation_set)
test_predictions = linear_model.predict(test_set)
# Model evaluation
mse = mean_squared_error(validation_labels, validation_predictions)
r2 = r2_score(validation_labels, validation_predictions)
# test case
mse_test = mean_squared_error(test_labels, test_predictions)
r2_test = r2_score(validation_labels, validation_predictions)
# Outcomes
print("Model coefficients :", linear_model.coef_)
print("Ordinate at origin :", linear_model.intercept_)
print("Mean square error (MSE) on the validation set :", mse)
print("R² score on validation set :", r2)

print("Mean square error (MSE) on the test set :", mse_test)
print("R² score on test set :", r2_test)
```

```
Model coefficients : [0.0442964  0.00127457 0.00138088 0.00339714 0.00062978
0.0066761
 0.15617054 0.0099289 ]
Ordinate at origin : -0.8038003713960418
Mean square error (MSE) on the validation set : 0.1489435251552441
R² score on validation set : 0.3411858794216768
Mean square error (MSE) on the test set : 0.14278585741240907
R² score on test set : 0.3411858794216768
```

Conclusion case 1 :

Looking at this result, the linear regression model explains **34%** of the data set R^2 = 0.34. This leaves more than **60%** of diabetes cases unexplained. What's more, of the **34%** explained, the model makes an average of **14%** errors.

So, to improve this model, we'd need more data, which we don't have. We will therefore test other models.

Case 2: Logistic regression

[47]:
```
# Initialization of the logistic regression model
logistic_model = LogisticRegression(max_iter=1000, random_state=42)

# Training the model on the training set
logistic_model.fit(train_set, train_labels)
```

```python
# Predictions on the validation set and test set
validation_predictions = logistic_model.predict(validation_set)
test_predictions = logistic_model.predict(test_set)

# Model evaluation on validation set
accuracy = accuracy_score(validation_labels, validation_predictions)
conf_matrix = confusion_matrix(validation_labels, validation_predictions)
class_report = classification_report(validation_labels, validation_predictions)

# Model evaluation on test set
accuracy_test = accuracy_score(test_labels, test_predictions)
conf_matrix_test = confusion_matrix(test_labels, test_predictions)
class_report_test = classification_report(test_labels, test_predictions)

# Displaying results for validation set
print("Accuracy on the validation set:", accuracy)
print("\nConfusion matrix:\n", conf_matrix)
print("\nClassification report:\n", class_report)

# Displaying results for test set
print("Accuracy on the test set:", accuracy_test)
print("\nConfusion matrix:\n", conf_matrix_test)
print("\nClassification report:\n", class_report_test)
```

```
Accuracy on the validation set: 0.7795555555555556

Confusion matrix:
 [[1319  154]
 [ 342  435]]

Classification report:
              precision    recall  f1-score   support

           0       0.79      0.90      0.84      1473
           1       0.74      0.56      0.64       777

    accuracy                           0.78      2250
   macro avg       0.77      0.73      0.74      2250
weighted avg       0.77      0.78      0.77      2250

Accuracy on the test set: 0.7915555555555556

Confusion matrix:
 [[1365  167]
 [ 302  416]]

Classification report:
              precision    recall  f1-score   support
```

```
              0       0.82      0.89      0.85      1532
              1       0.71      0.58      0.64       718

       accuracy                           0.79      2250
      macro avg       0.77      0.74      0.75      2250
   weighted avg       0.79      0.79      0.79      2250
```

2.3 #### Conclusion Cas 2:

Rappel Matrice de confusion:

	Prédiction: Positif	Prédiction: Négatif
Réel: Positif	Vrai Positif (VP)	Faux Négatif (FN)
Réel: Négatif	Faux Positif (FP)	Vrai Négatif (VN)

1. Precision=VN/(VP +FP):

- Plus elle est élevé, plus le modèle de Machine Learning minimise le nombre de Faux Positif.
- Quand la précision est haute, cela veut dire que la majorité des prédictions positives du modèle sont des positifs bien prédit.

2. recall=VP/(VP +FN):

- Plus il est élevé, plus le modèle de Machine Learning maximise le nombre de Vrai Positif.

Mais attention, cela ne veut pas dire que le modèle ne se trompe pas.

- Quand le recall est haut, cela veut plutôt dire qu'il ne ratera aucun positif. Néanmoins cela ne donne aucune information sur sa qualité de prédiction sur les négatifs.

3. F1 Score=2*(recall**precision /(recall+precision)) :

- Plus le F1 Score est élevé, plus le modèle est performant.

Source: https://inside-machinelearning.com/recall-precision-f1-score/

En analysant le rapport de ce résultat, nous obtenons un **recall de 78%**, une **précision de 78 %** ,f1-score **77%** et un **taux de vérités de 78 %**, laissant **32 % des cas non expliqués**.

Par conséquent, ce modèle ne semble pas adapté pour prédire les cas de diabète.

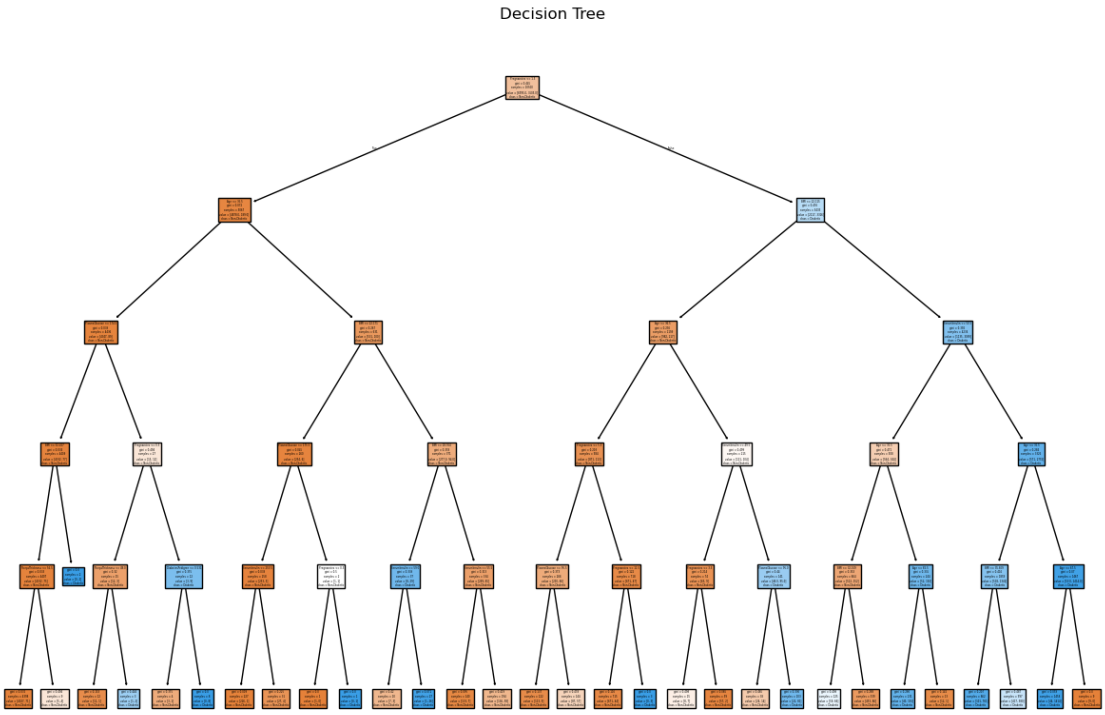
Case 3: Decision tree

[48]:
```
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, confusion_matrix,␣
 ↪classification_report
from sklearn.tree import plot_tree
import matplotlib.pyplot as plt
```

[49]:
```
# Initialization of the decision tree model
decision_tree_model = DecisionTreeClassifier(random_state=42, max_depth=5)

# Training the model on the training set
decision_tree_model.fit(train_set, train_labels)

# Predictions on the validation and test sets
validation_predictions = decision_tree_model.predict(validation_set)
test_predictions = decision_tree_model.predict(test_set)

# Model evaluation on the validation set
accuracy = accuracy_score(validation_labels, validation_predictions)
conf_matrix = confusion_matrix(validation_labels, validation_predictions)
class_report = classification_report(validation_labels, validation_predictions)

# Model evaluation on the test set
accuracy_test = accuracy_score(test_labels, test_predictions)
conf_matrix_test = confusion_matrix(test_labels, test_predictions)
class_report_test = classification_report(test_labels, test_predictions)

# Displaying results for the validation set
print("Accuracy on the validation set:", accuracy)
print("\nConfusion matrix:\n", conf_matrix)
print("\nClassification report:\n", class_report)

# Displaying results for the test set
print("Accuracy on the test set:", accuracy_test)
print("\nConfusion matrix:\n", conf_matrix_test)
print("\nClassification report:\n", class_report_test)

# Visualization of the decision tree
plt.figure(figsize=(15, 10))
plot_tree(decision_tree_model, feature_names=train_set.columns,␣
 ↪class_names=['Non-Diabetic', 'Diabetic'], filled=True)
plt.title("Decision Tree")
plt.show()
```

```
Accuracy on the validation set: 0.8977777777777778

Confusion matrix:
 [[1345  128]
 [ 102  675]]

Classification report:
              precision    recall  f1-score   support

           0       0.93      0.91      0.92      1473
           1       0.84      0.87      0.85       777
```

```
    accuracy                           0.90      2250
   macro avg       0.89      0.89      0.89      2250
weighted avg       0.90      0.90      0.90      2250

Accuracy on the test set: 0.888

Confusion matrix:
 [[1371  161]
 [  91  627]]

Classification report:
              precision    recall  f1-score   support

           0       0.94      0.89      0.92      1532
           1       0.80      0.87      0.83       718

    accuracy                           0.89      2250
   macro avg       0.87      0.88      0.87      2250
weighted avg       0.89      0.89      0.89      2250
```



Conclusion cas 3: En analysant le rapport de ce résultat, nous obtenons un **recall de 90%**, une

précision de 90 % ,f1-score **90%** , laissant **10 % des cas non expliqués**.

Par conséquent, ce modèle semble pas adapté pour prédire les cas de diabète.

Cas 4: SVM

[50]:
```
def evaluate_svm_kernels(train_set,␣
↪train_labels,validation_set,validation_labels, kernels=['linear', 'rbf',␣
↪'poly', 'sigmoid'], C_values=0.1):
    """
    Boucle sur différents noyaux SVM et valeurs de C, puis stocke les résultats␣
↪dans un DataFrame.

    Args:
        X (array): Features
        y (array): Target labels
        z (array): Validation labels
        w (array): Validation set
        kernels (list): Liste des noyaux à tester
        C_values (list): Liste des valeurs de C à tester

    Returns:
        pd.DataFrame: DataFrame avec accuracy, kernel et valeur de C
    """
    results = []

    # Séparer les données en ensemble d'entraînement et de test
    # Boucle sur les noyaux et les valeurs de C
    for kernel in kernels:
        # Créer et entraîner le modèle SVM
        model = SVC(kernel=kernel, C=C_values, gamma='scale', random_state=42)
        model.fit(train_set, train_labels)

        # Prédictions et évaluation
        y_pred = model.predict(validation_set)
        accuracy = accuracy_score(validation_labels, y_pred)

        # Stocker les résultats
        results.append({'Kernel': kernel, 'C': C_values, 'Accuracy': accuracy})

    # Convertir les résultats en DataFrame
    df_results = pd.DataFrame(results)
    return df_results
```

[51]:
```
#␣
↪vm_df_results=evaluate_svm_kernels(X=train_set,y=train_labels,X_test=validation_labels,y_te
```

[52]:
```
# # kernels=['linear', 'rbf', 'poly', 'sigmoid'],C_values=[0.1, 1, 10, 100]
# C_values=[0.1, 1, 10, 100]
# vm_df_results_list=pd.DataFrame()
# for c_ in C_values:
#   ␣
 ↪vm_df_results=evaluate_svm_kernels(train_set=train_set,train_labels=train_labels,validation
#   vm_df_results_list= pd.concat([vm_df_results, vm_df_results_list],␣
 ↪ignore_index=True)
```

SVM for C=1

[53]:
```
vm_df_results_1=evaluate_svm_kernels(train_set=train_set,train_labels=train_labels,validation_
```

SVM for C=10

[54]:
```
vm_df_results_10=evaluate_svm_kernels(train_set=train_set,train_labels=train_labels,validation
```

2.3.1 SVM for C=100

[55]:
```
vm_df_results_100=evaluate_svm_kernels(train_set=train_set,train_labels=train_labels,validatio
```

[56]:
```
validation_set.columns
```

[56]:
```
Index(['Pregnancies', 'PlasmaGlucose', 'DiastolicBloodPressure',
       'TricepsThickness', 'SerumInsulin', 'BMI', 'DiabetesPedigree', 'Age'],
      dtype='object')
```

[57]:
```
# Afficher les resultats
display(vm_df_results_1)
display(vm_df_results_10)
display(vm_df_results_100)
```

	Kernel	C	Accuracy
0	linear	1	0.777333
1	rbf	1	0.803556
2	poly	1	0.772889
3	sigmoid	1	0.579556

	Kernel	C	Accuracy
0	linear	10	0.782222
1	rbf	10	0.817333
2	poly	10	0.790222
3	sigmoid	10	0.579111

	Kernel	C	Accuracy
0	linear	100	0.788444
1	rbf	100	0.832889
2	poly	100	0.802222
3	sigmoid	100	0.579111

Conclusion cas 4:

Analyzing these results, the best-performing model is the one with an rbf kernel and c=100, which has a success rate of 83%.

Case 5: RN With 3 simple layer

[58]:
```
# Normalyse data
scaler = StandardScaler()
X_train = scaler.fit_transform(train_set)
X_val = scaler.transform(validation_set)
X_test = scaler.transform(test_set)

# No normalisation for etiquette
y_train = train_labels
y_val = validation_labels
y_test = test_labels
# Model layer(couche)
model = Sequential([
    Dense(10, activation='relu', input_shape=(X_train.shape[1],)),
    Dense(8, activation='relu'),
    Dense(3, activation='softmax')
])


model.compile(optimizer='adam', loss='sparse_categorical_crossentropy',␣
 ↪metrics=['accuracy'])
history =model.fit(X_train, y_train, epochs=50, batch_size=5, verbose=1,␣
 ↪validation_data=(X_val, y_val))
```

```
/home/peyanan/miniconda3/envs/dsti_ml_env/lib/python3.12/site-
packages/keras/src/layers/core/dense.py:87: UserWarning: Do not pass an
`input_shape`/`input_dim` argument to a layer. When using Sequential models,
prefer using an `Input(shape)` object as the first layer in the model instead.
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
2025-03-12 12:50:45.839413: E
external/local_xla/xla/stream_executor/cuda/cuda_platform.cc:51] failed call to
cuInit: INTERNAL: CUDA error: Failed call to cuInit: UNKNOWN ERROR (303)

Epoch 1/50
2100/2100             12s 4ms/step -
accuracy: 0.7067 - loss: 0.6211 - val_accuracy: 0.8036 - val_loss: 0.4139
Epoch 2/50
2100/2100             7s 3ms/step -
accuracy: 0.8119 - loss: 0.3859 - val_accuracy: 0.8440 - val_loss: 0.3356
Epoch 3/50
2100/2100             6s 3ms/step -
accuracy: 0.8456 - loss: 0.3280 - val_accuracy: 0.8667 - val_loss: 0.2994
Epoch 4/50
2100/2100             7s 3ms/step -
accuracy: 0.8654 - loss: 0.3016 - val_accuracy: 0.8747 - val_loss: 0.2910
```

```
Epoch 5/50
2100/2100            7s 3ms/step -
accuracy: 0.8689 - loss: 0.2954 - val_accuracy: 0.8769 - val_loss: 0.2843
Epoch 6/50
2100/2100            11s 5ms/step -
accuracy: 0.8721 - loss: 0.2919 - val_accuracy: 0.8853 - val_loss: 0.2733
Epoch 7/50
2100/2100            12s 5ms/step -
accuracy: 0.8807 - loss: 0.2846 - val_accuracy: 0.8831 - val_loss: 0.2741
Epoch 8/50
2100/2100            16s 8ms/step -
accuracy: 0.8846 - loss: 0.2759 - val_accuracy: 0.8853 - val_loss: 0.2706
Epoch 9/50
2100/2100            7s 4ms/step -
accuracy: 0.8839 - loss: 0.2696 - val_accuracy: 0.8867 - val_loss: 0.2707
Epoch 10/50
2100/2100            10s 5ms/step -
accuracy: 0.8898 - loss: 0.2666 - val_accuracy: 0.8827 - val_loss: 0.2702
Epoch 11/50
2100/2100            15s 7ms/step -
accuracy: 0.8827 - loss: 0.2706 - val_accuracy: 0.8813 - val_loss: 0.2764
Epoch 12/50
2100/2100            13s 6ms/step -
accuracy: 0.8822 - loss: 0.2657 - val_accuracy: 0.8827 - val_loss: 0.2755
Epoch 13/50
2100/2100            7s 3ms/step -
accuracy: 0.8837 - loss: 0.2664 - val_accuracy: 0.8876 - val_loss: 0.2664
Epoch 14/50
2100/2100            12s 6ms/step -
accuracy: 0.8839 - loss: 0.2689 - val_accuracy: 0.8858 - val_loss: 0.2634
Epoch 15/50
2100/2100            15s 7ms/step -
accuracy: 0.8862 - loss: 0.2653 - val_accuracy: 0.8822 - val_loss: 0.2753
Epoch 16/50
2100/2100            12s 6ms/step -
accuracy: 0.8914 - loss: 0.2598 - val_accuracy: 0.8867 - val_loss: 0.2660
Epoch 17/50
2100/2100            14s 6ms/step -
accuracy: 0.8862 - loss: 0.2704 - val_accuracy: 0.8893 - val_loss: 0.2592
Epoch 18/50
2100/2100            12s 6ms/step -
accuracy: 0.8840 - loss: 0.2694 - val_accuracy: 0.8858 - val_loss: 0.2600
Epoch 19/50
2100/2100            12s 6ms/step -
accuracy: 0.8866 - loss: 0.2649 - val_accuracy: 0.8911 - val_loss: 0.2568
Epoch 20/50
2100/2100            13s 6ms/step -
accuracy: 0.8958 - loss: 0.2487 - val_accuracy: 0.8933 - val_loss: 0.2540
```

```
Epoch 21/50
2100/2100            8s 4ms/step -
accuracy: 0.8885 - loss: 0.2579 - val_accuracy: 0.8960 - val_loss: 0.2531
Epoch 22/50
2100/2100            10s 5ms/step -
accuracy: 0.9012 - loss: 0.2402 - val_accuracy: 0.8933 - val_loss: 0.2484
Epoch 23/50
2100/2100            8s 4ms/step -
accuracy: 0.9017 - loss: 0.2414 - val_accuracy: 0.8924 - val_loss: 0.2521
Epoch 24/50
2100/2100            4s 2ms/step -
accuracy: 0.8963 - loss: 0.2468 - val_accuracy: 0.8969 - val_loss: 0.2458
Epoch 25/50
2100/2100            6s 3ms/step -
accuracy: 0.8976 - loss: 0.2366 - val_accuracy: 0.8911 - val_loss: 0.2521
Epoch 26/50
2100/2100            7s 3ms/step -
accuracy: 0.8972 - loss: 0.2433 - val_accuracy: 0.8796 - val_loss: 0.2718
Epoch 27/50
2100/2100            6s 3ms/step -
accuracy: 0.9025 - loss: 0.2368 - val_accuracy: 0.8964 - val_loss: 0.2452
Epoch 28/50
2100/2100            7s 3ms/step -
accuracy: 0.9024 - loss: 0.2318 - val_accuracy: 0.8947 - val_loss: 0.2460
Epoch 29/50
2100/2100            5s 3ms/step -
accuracy: 0.9027 - loss: 0.2360 - val_accuracy: 0.8991 - val_loss: 0.2420
Epoch 30/50
2100/2100            6s 3ms/step -
accuracy: 0.9000 - loss: 0.2298 - val_accuracy: 0.8920 - val_loss: 0.2475
Epoch 31/50
2100/2100            6s 3ms/step -
accuracy: 0.9065 - loss: 0.2295 - val_accuracy: 0.8973 - val_loss: 0.2396
Epoch 32/50
2100/2100            7s 3ms/step -
accuracy: 0.9008 - loss: 0.2379 - val_accuracy: 0.8951 - val_loss: 0.2414
Epoch 33/50
2100/2100            7s 4ms/step -
accuracy: 0.9068 - loss: 0.2358 - val_accuracy: 0.8951 - val_loss: 0.2410
Epoch 34/50
2100/2100            6s 3ms/step -
accuracy: 0.9037 - loss: 0.2270 - val_accuracy: 0.9009 - val_loss: 0.2366
Epoch 35/50
2100/2100            7s 3ms/step -
accuracy: 0.9009 - loss: 0.2284 - val_accuracy: 0.8973 - val_loss: 0.2433
Epoch 36/50
2100/2100            6s 3ms/step -
accuracy: 0.8987 - loss: 0.2407 - val_accuracy: 0.9022 - val_loss: 0.2397
```

```
Epoch 37/50
2100/2100            7s 3ms/step -
accuracy: 0.9085 - loss: 0.2276 - val_accuracy: 0.9036 - val_loss: 0.2339
Epoch 38/50
2100/2100            8s 4ms/step -
accuracy: 0.9081 - loss: 0.2255 - val_accuracy: 0.9004 - val_loss: 0.2364
Epoch 39/50
2100/2100            5s 3ms/step -
accuracy: 0.9053 - loss: 0.2277 - val_accuracy: 0.9022 - val_loss: 0.2431
Epoch 40/50
2100/2100            6s 3ms/step -
accuracy: 0.9036 - loss: 0.2244 - val_accuracy: 0.9044 - val_loss: 0.2319
Epoch 41/50
2100/2100            6s 3ms/step -
accuracy: 0.9064 - loss: 0.2209 - val_accuracy: 0.9049 - val_loss: 0.2294
Epoch 42/50
2100/2100            7s 3ms/step -
accuracy: 0.9069 - loss: 0.2264 - val_accuracy: 0.9040 - val_loss: 0.2299
Epoch 43/50
2100/2100            7s 3ms/step -
accuracy: 0.9100 - loss: 0.2245 - val_accuracy: 0.9040 - val_loss: 0.2346
Epoch 44/50
2100/2100            6s 3ms/step -
accuracy: 0.9103 - loss: 0.2220 - val_accuracy: 0.9071 - val_loss: 0.2313
Epoch 45/50
2100/2100            6s 3ms/step -
accuracy: 0.9109 - loss: 0.2154 - val_accuracy: 0.9036 - val_loss: 0.2261
Epoch 46/50
2100/2100            6s 3ms/step -
accuracy: 0.9133 - loss: 0.2196 - val_accuracy: 0.9067 - val_loss: 0.2299
Epoch 47/50
2100/2100            6s 3ms/step -
accuracy: 0.9083 - loss: 0.2225 - val_accuracy: 0.9058 - val_loss: 0.2309
Epoch 48/50
2100/2100            6s 3ms/step -
accuracy: 0.9120 - loss: 0.2185 - val_accuracy: 0.9013 - val_loss: 0.2335
Epoch 49/50
2100/2100            5s 2ms/step -
accuracy: 0.9119 - loss: 0.2136 - val_accuracy: 0.9018 - val_loss: 0.2313
Epoch 50/50
2100/2100            7s 3ms/step -
accuracy: 0.9076 - loss: 0.2249 - val_accuracy: 0.8991 - val_loss: 0.2321
```

5.1) Verify the overfiting or underfiting Some tips to find each case.

3 1 Overfiting

Écart entre la précision ou la perte sur train et validation:

- Précision très élevée sur l'entraînement
- Perte faible sur l'entraînement

Courbes d'entraînement et validation divergentes

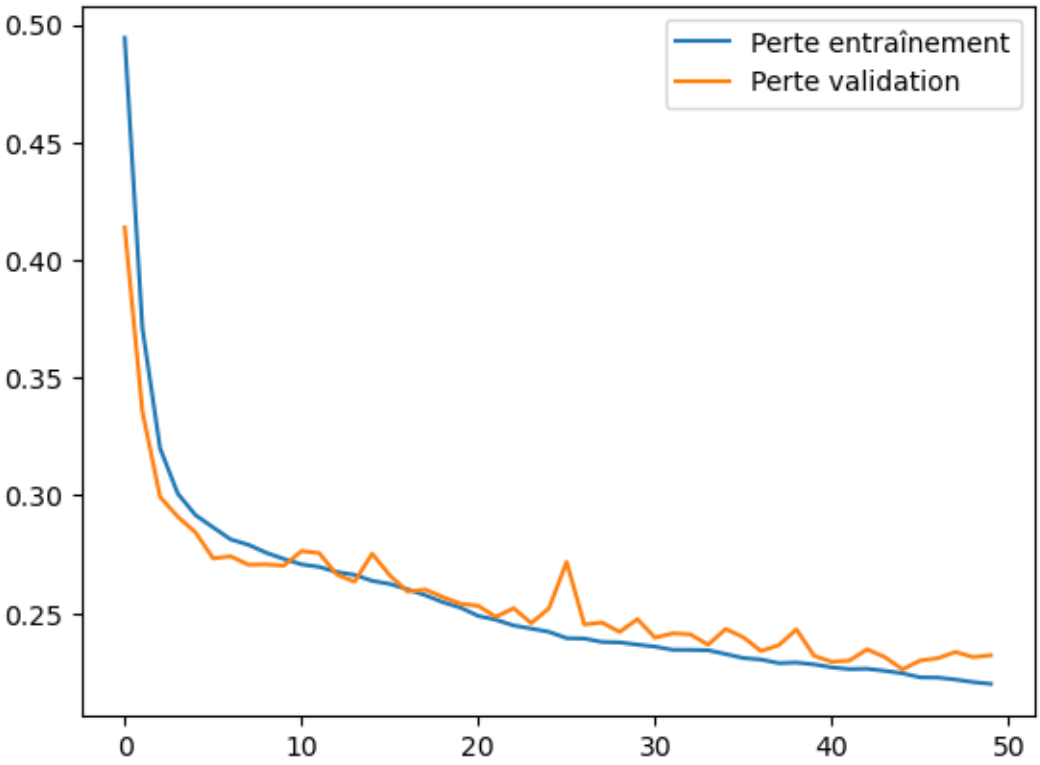
Performance très faible sur le jeu de test : Si ton modèle performe bien sur le train mais mal sur le test, il est surentraîné.

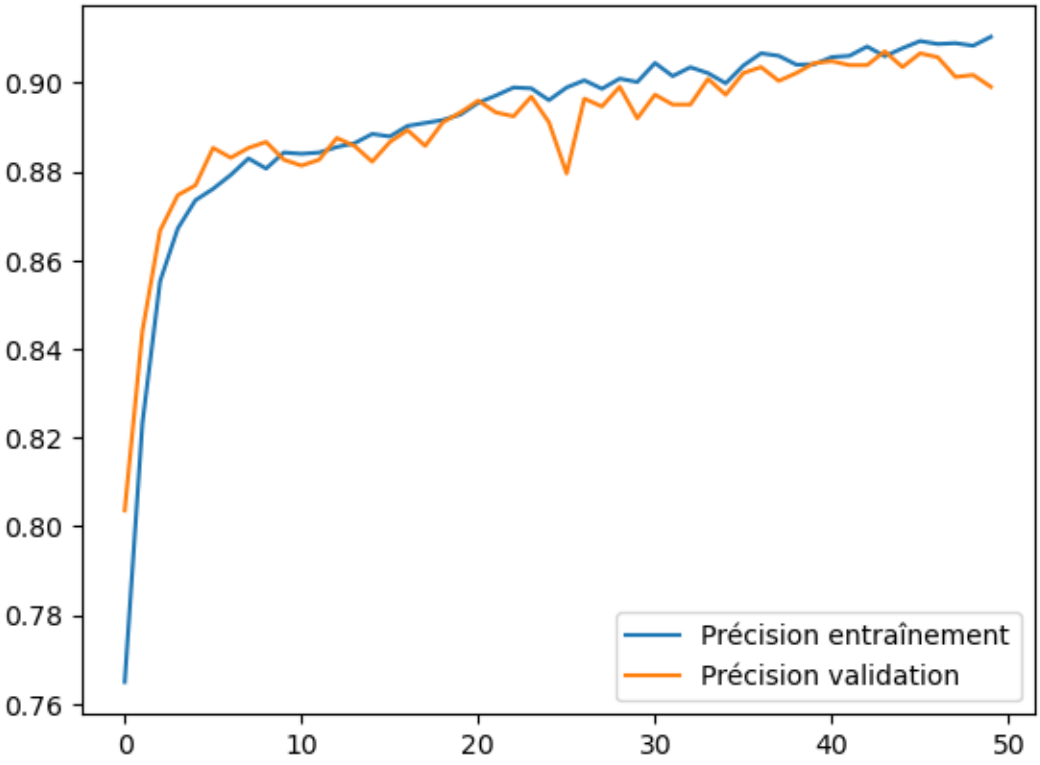
4 2- Underfiting

Précision faible sur train et validation : Même après plusieurs époques, le modèle n'arrive pas à bien prédire, et la précision reste basse sur les deux ensembles. Perte élevée sur train et validation : La fonction de perte reste élevée et ne s'améliore pas beaucoup au fil des époques. Pas de sur-ajustement aux données d'entraînement : Contrairement au sur-entraînement, ici les performances restent mauvaises partout — le modèle n'a même pas mémorisé correctement les données d'entraînement.

[59]:
```
# Tracer la perte
print(history.history.keys())
plt.plot(history.history['loss'], label='Perte entraînement')
plt.plot(history.history['val_loss'], label='Perte validation')
plt.legend()
plt.show()

# Tracer la précision
plt.plot(history.history['accuracy'], label='Précision entraînement')
plt.plot(history.history['val_accuracy'], label='Précision validation')
plt.legend()
plt.show()
```

```
dict_keys(['accuracy', 'loss', 'val_accuracy', 'val_loss'])
```


Perte entraînement
Perte validation
0.50
0.45
0.40
0.35
0.30
0.25
0
10
20
30
40
50


Précision entraînement
Précision validation
0.90
0.88
0.86
0.84
0.82
0.80
0.78
0.76
0
10
20
30
40
50

Evaluate the model

[60]:
```
# Évaluer le modèle sur le jeu de test
loss, accuracy = model.evaluate(X_test, y_test)
print(f'Accuracy of  test set: {accuracy:.2f}')
```

```
71/71             1s 3ms/step -
accuracy: 0.8881 - loss: 0.2693
Accuracy of  test set: 0.90
```

5 - Conclusion

By observing the evolution of the loss function, we can see that there is no divergence, which means that there is neither overlearning nor underlearning. As a result, the model achieves 90% accuracy.

[61]:
```
# print(loss)
```

4.0.1 6- KNeighborsClassifier

[62]:
```
knn = KNeighborsClassifier(n_neighbors=3)
knn.fit(train_set, train_labels)
validation_predictions = knn.predict(validation_set)
test_predictions = knn.predict(test_set)

accuracy_val=accuracy_score(validation_labels,validation_predictions)
conf_matrix_val=confusion_matrix(validation_labels,validation_predictions)
classification_reg_val =␣
 ↪classification_report(validation_labels,validation_predictions)
# test
accuracy_test=accuracy_score(test_labels,test_predictions)
conf_matrix_test=confusion_matrix(test_labels,test_predictions)
classification_reg_test = classification_report(test_labels,test_predictions)
#
print("accurcy of validation:", accuracy_val)
print("confusion matrix of validation:", conf_matrix_val)
print("classification of validation:",classification_reg_val)
#
print("accurcy of test:", accuracy_test)
print("confusion matrix of test:", conf_matrix_test)
print("classification of test:",classification_reg_test)
```

```
accurcy of validation: 0.8346666666666667
confusion matrix of validation: [[1316  157]
 [ 215  562]]
classification of validation:               precision    recall  f1-score
support
```

```
              0       0.86      0.89      0.88      1473
              1       0.78      0.72      0.75       777

    accuracy                           0.83      2250
   macro avg       0.82      0.81      0.81      2250
weighted avg       0.83      0.83      0.83      2250

accurcy of test: 0.8391111111111111
confusion matrix of test: [[1371  161]
 [ 201  517]]
classification of test:               precision    recall  f1-score   support

              0       0.87      0.89      0.88      1532
              1       0.76      0.72      0.74       718

    accuracy                           0.84      2250
   macro avg       0.82      0.81      0.81      2250
weighted avg       0.84      0.84      0.84      2250
```

Conclusion 6: The k-NN model performs similarly on the validation and test sets, with an overall precision of around 83-84%. It classifies class 0 better (higher precision, recall and F1-score values) than class 1, which could indicate an imbalance or difficulty in correctly recognizing class 1. The model shows good generalizability, as performance is close between the validation and test sets.

4.1 7- GradientBoostingClassifier

This algorithm builds an additive model in a forward stage-wise fashion; it allows for the optimization of arbitrary differentiable loss functions. In each stage n_classes_ regression trees are fit on the negative gradient of the loss function, e.g. binary or multiclass log loss. Binary classification is a special case where only a single regression tree is induced.

[63]:
```
gb = GradientBoostingClassifier(n_estimators=100, learning_rate=0.1,␣
 ↪max_depth=3, random_state=42)
gb.fit(train_set, train_labels)
validation_predictions = gb.predict(validation_set)
test_predictions = gb.predict(test_set)


accuracy_val =accuracy_score(validation_labels,validation_predictions)
conf_matrix_val=confusion_matrix(validation_labels,validation_predictions)
classification_reg_val =␣
 ↪classification_report(validation_labels,validation_predictions)

accuracy_test =accuracy_score(test_labels,test_predictions)
conf_matrix_test=confusion_matrix(test_labels,test_predictions)
classification_reg_test = classification_report(test_labels,test_predictions)
```

```
print("accurcy of validation", accuracy_val)
print("confusion matrix of validation:", conf_matrix_val)
print("classification of validation:",classification_reg_val )
#
print("accurcy of test", accuracy_test)
print("confusion matrix of test:", conf_matrix_test)
print("classification of test:",classification_reg_test )
```

```
accurcy of validation 0.9524444444444444
confusion matrix of validation: [[1429   44]
 [  63  714]]
classification of validation:               precision    recall  f1-score
support

           0       0.96      0.97      0.96      1473
           1       0.94      0.92      0.93       777

    accuracy                           0.95      2250
   macro avg       0.95      0.94      0.95      2250
weighted avg       0.95      0.95      0.95      2250

accurcy of test 0.9426666666666667
confusion matrix of test: [[1474   58]
 [  71  647]]
classification of test:               precision    recall  f1-score   support

           0       0.95      0.96      0.96      1532
           1       0.92      0.90      0.91       718

    accuracy                           0.94      2250
   macro avg       0.94      0.93      0.93      2250
weighted avg       0.94      0.94      0.94      2250
```

Conclusion 7: Gradient Boosting performs significantly better than the previous k-NN model. Overall accuracy exceeds 94% on both sets, with high F1 scores for both classes. The model also seems to generalize well, as results are consistent between validation and testing. Class 0 is still slightly better recognized than class 1, but the gap is reduced. This model seems more efficient and balanced.

4.2 8- Random forest

[64]:
```
# Initialiser le Random Forest
rf = RandomForestClassifier(n_estimators=100, random_state=42)

# Entraîner le modèle
rf.fit(train_set, train_labels)
```

```
# Prédictions et évaluation sur l'ensemble de validation
y_val_pred = rf.predict(validation_set)
val_accuracy = accuracy_score(validation_labels, y_val_pred)
print(f'Accuracy on validation set: {val_accuracy:.4f}')

# Prédictions et évaluation sur l'ensemble de test
y_test_pred = rf.predict(test_set)
test_accuracy = accuracy_score(y_test, y_test_pred)
print(f'Accuracy on test set: {test_accuracy:.4f}')
```

```
Accuracy on validation set: 0.9329
Accuracy on test set: 0.9338
```

4.3 Final conclusion:

After several series of tests with different algorithms, we obtained the best result, achieving an accuracy of 95.24% in the prediction of the diabetic variable. However, the available variables do not provide a 100% explanation of the diabetic phenomenon, and we will restrict ourselves to the features provided.

Thus, the best-performing algorithm is a classifier, which is not surprising given that our problem was one of classification. The chosen model is therefore Gradient Boosting.

4.4 Model saving

[66]:
```
import joblib
#The best model
joblib.dump(gb, 'grandiantBoostingClassifier.pkl')
print("The model  saved !")
```

```
The model  saved !
```

[ ]:
```

```